

GenCore version 5.1.6
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OM protein - protein search, using bw model

Run on: November 2, 2005, 10:55:28 / Search time 43 seconds

(without alignment)

612.817 Million cell updates/sec

Title: US-09-905-075-2

Perfect score: 2005

Sequence: 1 MRLPRALGLPLLLPLLP.....AARATRGESPTQLPSRDL 353

Scoring table: BLOSUM62

Gap: 10.0, Gapex: 0.5

Search: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: Issued Patents AA*

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Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUPPMA185

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104	221	11.0	1347	US-09-561-403-14	Sequence 14, Appl 1	177	201	10.0	383	1	US-08-451-245-2	Sequence 2, Appl 1
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152	209.5	10.4	448	US-09-576-165-34	Sequence 34, Appl 1	223	196	9.8	816	3	US-09-565-538-37	Sequence 37, Appl 1
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158	208.5	10.4	1055	US-09-855-722-2	Sequence 2, Appl 1	229	195.5	9.8	683	3	US-08-402-553-2	Sequence 2, Appl 1
159	207	10.3	1065	US-09-855-722-2	Sequence 2, Appl 1	230	195.5	9.8	683	3	US-08-402-553-2	Sequence 2, Appl 1
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GenCore version 5.1.6

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Run on: November 2, 2005, 10:11:35; Search time 167 Seconds
(without alignment)

817.523 Million cell updates/sec

Title: US-09-905-075-2

Perfect score: 2005
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Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 2105692 seqs, 36676081 residues
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Minimum DB seq length: 0
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Post-processing: Minimum Match 100
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Filter: 100 summaries

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8: Geneseq.20040.*

Pred. No. 10 the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of SUMMARIES

No. 1 Score Match Length DB ID Description

RESULT 1
ID AAV05283 standard; protein; 353 AA.
DE EGP-11ke homologue PRO211.
PN MO9914327-A2.
PD 25-MAR-1999.

PA (GRTN) GENENTECH INC.
Query Match 100.0%; Score 2005; DB 2; Length 353;
Best Local Similarity 100.0%; Pred. No. 6e-131;

RESULT 2
ID AAV09064 standard; protein; 353 AA.
DE Human EGP-11ke homologue protein (PRO217) encoded by DNA2292 cDNA.
PN MO9914441-A2.
PD 25-MAR-1999.

PA (GRTN) GENENTECH INC.
Query Match 100.0%; Score 2005; DB 2; Length 353;
Best Local Similarity 100.0%; Pred. No. 6e-131;

RESULT 3
ID AAT13344 standard; protein; 353 AA.
DE Amino acid sequence of protein PRO211.
PN MO9914428-A2.
PD 25-MAR-1999.

PA (GRTN) GENENTECH INC.
Query Match 100.0%; Score 2005; DB 2; Length 353;
Best Local Similarity 100.0%; Pred. No. 6e-131;

RESULT 4
ID AAV83224 standard; protein; 353 AA.
DE PRO211 Polypeptide.
PN MO300021996-A2.
PD 20-APR-2000.

PA (GRTN) GENENTECH INC.
Query Match 100.0%; Score 2005; DB 3; Length 353;
Best Local Similarity 100.0%; Pred. No. 6e-131;

RESULT 5
ID AAV83224 standard; protein; 353 AA.
DE PRO211 Polypeptide.
PN MO300021996-A2.
PD 20-APR-2000.

PA (GRTN) GENENTECH INC.
Query Match 100.0%; Score 2005; DB 3; Length 353;
Best Local Similarity 100.0%; Pred. No. 6e-131;

RESULT 6
ID AAV83224 standard; protein; 353 AA.
DE PRO211 Polypeptide.
PN MO300021996-A2.
PD 20-APR-2000.

PA (GRTN) GENENTECH INC.
Query Match 100.0%; Score 2005; DB 3; Length 353;
Best Local Similarity 100.0%; Pred. No. 6e-131;

RESULT 7
ID AAV83224 standard; protein; 353 AA.
DE PRO211 Polypeptide.
PN MO300021996-A2.
PD 20-APR-2000.

PA (GRTN) GENENTECH INC.
Query Match 100.0%; Score 2005; DB 3; Length 353;
Best Local Similarity 100.0%; Pred. No. 6e-131;

DE Human PRO211 protein.

DE 202001576-A2.
DE 202001576-A2.
PA (GRTN) GENENTECH INC.

Query Match 100.0%; Score 2005; DB 3; Length 353;
Best Local Similarity 100.0%; Pred. No. 6e-131;

RESULT 7
ID AAB80212 standard; protein; 353 AA.
DE Human PRO211 protein.
PN MO200104311-A1.
PD 18-JAN-2001.

PA (GRTN) GENENTECH INC.
Query Match 100.0%; Score 2005; DB 4; Length 353;
Best Local Similarity 100.0%; Pred. No. 6e-131;

RESULT 8
ID AAB81231 standard; protein; 353 AA.
DE Human TMO2 331 protein.
PN MO200106638-A2.
PD 04-JAN-2001.

PA (MIL-) MILLENNIUM PHARM INC.
Query Match 100.0%; Score 2005; DB 4; Length 353;
Best Local Similarity 100.0%; Pred. No. 6e-131;

RESULT 9
ID AAV12319 standard; protein; 353 AA.
DE Human PRO211 polypeptide sequence.
PN MO200140466-A2.
PD 07-JUN-2001.

PA (GRTN) GENENTECH INC.
Query Match 100.0%; Score 2005; DB 4; Length 353;
Best Local Similarity 100.0%; Pred. No. 6e-131;

RESULT 10
ID AAB53075 standard; protein; 353 AA.
DE Human angiotensin-II-associated protein PRO211, SEQ ID NO:57.
PN MO200053753-A2.
PD 14-SEP-2000.

PA (GRTN) GENENTECH INC.
Query Match 100.0%; Score 2005; DB 4; Length 353;
Best Local Similarity 100.0%; Pred. No. 6e-131;

RESULT 11
ID AAB53075 standard; protein; 353 AA.
DE Human angiotensin-II-associated protein PRO211, SEQ ID NO:57.
PN MO200053753-A2.
PD 14-SEP-2000.

PA (GRTN) GENENTECH INC.
Query Match 100.0%; Score 2005; DB 4; Length 353;
Best Local Similarity 100.0%; Pred. No. 6e-131;

RESULT 12
ID AAB71590 standard; protein; 353 AA.
DE Human PRO polypeptide #1.
PN US2002146709-A1.
PD 10-OCT-2002.

PA (GRTN) GENENTECH INC.
Query Match 100.0%; Score 2005; DB 6; Length 353;
Best Local Similarity 100.0%; Pred. No. 6e-131;

RESULT 13
ID ABO17763 standard; protein; 353 AA.
DE Novel human secreted and transmembrane protein PRO211.
PN US2003032156-A1.
PD 13-FEB-2003.

PA (GRTN) GENENTECH INC.
Query Match 100.0%; Score 2005; DB 6; Length 353;
Best Local Similarity 100.0%; Pred. No. 6e-131;

RESULT 14
ID ABB71445 standard; protein; 353 AA.
DE Human PRO211 polypeptide #1.
PN US2002182459-A1.
PD 19-DEC-2002.

PA (GRTN) GENENTECH INC.
Query Match 100.0%; Score 2005; DB 6; Length 353;
Best Local Similarity 100.0%; Pred. No. 6e-131;

RESULT 15
ID ABB81017 standard; protein; 353 AA.
DE Human PRO polypeptide #148.

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[illegible]

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OM protein - protein search, using sw model

Run on: November 2, 2005, 10:42:37 : Search time 176 Seconds

(Without alignment)
1027.068 Million cell updates/sec

Title: US-09-905-075-2

Perfect score: 2005
Sequence: 1 MRLPRALGLPLLLALLP.....AEAEATGESPQLPSRDL 353

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 01
Maximum Match 1001
Length filter 1500 summaries

Database: 1: uniprot_sprot.*
2: uniprot_trembl.*

Prod. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Seq	Match Length	ID	Description
1	2005	100.0	06XU1	06xui1 homo sapien
2	1995	99.5	06XU0	06xui0 homo sapien
3	1797	89.1	09BU47	09bu47 homo sapien
4	1533.5	76.5	09CYA0	09cy40 mus musculu
5	1481.5	73.9	060438	060438 citreulacu
6	1020.5	50.9	075XK6	075xk6 brachydanio
7	971.5	48.5	0202	02022 homo sapien
8	969	48.3	02021	02021 homo sapien
9	968.5	48.3	02020	02020 mus musculu
10	959.5	47.9	021X07	021x07 homo sapien
11	959.5	47.9	021X06	021x06 homo sapien
12	899	34.9	065584	065584 homo sapien
13	670	33.4	09VJ20	09vj20 dirosophila
14	655.5	32.7	0703P0	0703p0 anopheles g
15	599.5	29.9	09DPE9	09dpe9 oncorhynch
16	540	26.9	019267	019267 caenorhabd
17	423	21.1	08BY28	08by28 mus musculu
18	286.5	14.3	073715	073715 gallus galli
19	279.5	13.9	09BJ31	09bj31 elomx intes
20	279	13.9	07Y2P0	07y2p0 elmerita max
21	277.5	13.8	08W4E8	08w4e8 h. etabillu
22	274.5	13.6	08W4E7	08w4e7 h. etabillu
23	274.5	13.7	08W4E6	08w4e6 h. etabillu
24	274.5	13.7	08W4E5	08w4e5 h. etabillu
25	272	13.6	000558	000558 homo sapien
26	271.5	13.5	075412	075412 homo sapien
27	271	13.5	09B105	09b105 elmerita ten
28	270.5	13.5	088840	088840 boe laurus
29	270	13.5	088840	088840 boe laurus
30	268.5	13.4	088840	088840 boe laurus
31	268.5	13.4	088840	088840 boe laurus

32	268	13.4	1821	1	LTB2_HUMAN	014767 homo sapien
33	268	13.4	1821	2	Q6A294	06a294 mus musculu
34	266.5	13.3	1644	1	LTB4_MOUSE	084903 mus musculu
35	266.5	13.3	1644	2	LTB4_MOUSE	084901 mus musculu
36	266.5	13.3	2809	1	PBN1_HUMAN	075930 homo sapien
37	266.5	13.2	1842	1	LTB2_BOVIN	028019 boe laurus
38	263	13.1	708	2	P87363	087363 gallus galli
39	263	13.1	1877	1	PECK5_MOUSE	004592 mus musculu
40	262.5	13.1	1167	2	Q6KAT1	06kac1 mus musculu
41	262.5	13.1	1764	2	LTB2_RAT	035806 ratu8 norv
42	262.5	13.0	669	2	Q9W0F8	09w0f8 ratu8 norv
43	260.5	13.0	23015	2	075441	075441 homo sapien
44	260.5	13.0	3775	2	081018	081018 dirosophila
45	259.5	12.9	893	2	Q7WPF9	07wpf9 anopheles g
46	259.5	12.9	893	3	Q7WPF9	07wpf9 anopheles g
47	257.5	12.8	652	1	CD93_HUMAN	081241 homo sapien
48	257.5	12.8	705	1	PBL1_MOUSE	008879 mus musculu
49	256.5	12.8	1302	1	LTB3_HUMAN	09n815 homo sapien
50	256.5	12.8	1302	2	LTB3_HUMAN	09n815 homo sapien
51	256	12.8	1268	1	PBL1_MOUSE	061810 mus musculu
52	254.5	12.7	703	1	CD93_RAT	09e161 ratu8 norv
53	254	12.7	643	2	Q9V4B8	09v4b8 dirosophila
54	253.5	12.6	917	2	Q9V4B8	09v4b8 dirosophila
55	253	12.6	2585	2	Q23587	023587 caenorhabd
56	252.5	12.6	2871	1	PBN1_MOUSE	061354 mus musculu
57	252.5	12.6	2907	1	PBN2_MOUSE	061354 mus musculu
58	251.5	12.5	1814	1	LTB2_MOUSE	099158 mus musculu
59	251.5	12.5	2571	1	SBN1_MOUSE	008999 mus musculu
60	250	12.5	2571	2	SBN1_MOUSE	008999 mus musculu
61	250	12.5	3494	2	Q7LC53	07lc53 homo sapien
62	250	12.5	3523	2	Q60494	060494 homo sapien
63	249.5	12.4	2911	1	PBN2_HUMAN	09wuh9 ratu8 norv
64	249	12.4	2906	2	PECK5_HUMAN	09wuh9 ratu8 norv
65	248.5	12.4	1696	1	PECK5_BRACL	09wuh9 ratu8 norv
66	247	12.3	675	1	PPTS_RAT	053813 ratu8 norv
67	247	12.3	997	2	Q9UJ50	09uj50 mus musculu
68	247	12.3	1221	1	PBL2_MOUSE	091889 mus musculu
69	246.5	12.3	1368	2	Q9NH16	09nh16 mus musculu
70	246.5	12.3	1368	3	Q9NH16	09nh16 mus musculu
71	246.5	12.3	1368	4	Q9NH16	09nh16 mus musculu
72	245.5	12.2	1871	2	Q20911	020911 mus musculu
73	245.5	12.2	1871	3	Q20911	020911 mus musculu
74	244	12.2	733	2	Q25678	025678 dirosophila
75	244	12.2	971	2	Q6ZM11	06zm11 homo sapien
76	244	12.2	999	2	Q9NQ36	09nq36 homo sapien
77	244	12.2	1231	2	Q9N1U0	09n1u0 homo sapien
78	243	12.1	915	2	Q91VX0	091vx0 mus musculu
79	243	12.1	1231	2	Q91U11	091u11 homo sapien
80	242.5	12.1	1184	1	PBL2_HUMAN	081018 dirosophila
81	242.5	12.1	1184	2	PBL2_HUMAN	081018 dirosophila
82	241.5	12.0	1030	1	PBN1_MOUSE	061354 mus musculu
83	241.5	12.0	1030	2	PBN1_MOUSE	061354 mus musculu
84	241	12.0	561	2	Q91VX8	091vx8 mus musculu
85	240.5	12.0	1394	1	LTB3_HUMAN	09wuh9 ratu8 norv
86	240.5	12.0	1394	2	LTB3_HUMAN	09wuh9 ratu8 norv
87	240.5	12.0	1595	1	LTB3_HUMAN	09wuh9 ratu8 norv
88	239.5	11.9	561	2	Q6NV58	06nv58 mus musculu
89	239	11.9	497	2	Q72715	072715 homo sapien
90	239	11.9	528	2	Q9CX08	09cx08 mus musculu
91	239	11.9	676	1	PPTS_HUMAN	053813 ratu8 norv
92	239	11.9	1299	2	Q26489	026489 mus musculu
93	239	11.9	1299	3	Q26489	026489 mus musculu
94	239	11.9	1299	4	Q26489	026489 mus musculu
95	237	11.8	872	2	Q61W84	061w84 mus musculu
96	237	11.8	872	3	Q61W84	061w84 mus musculu
97	237	11.8	986	2	Q81W94	081w94 homo sapien
98	237	11.8	992	2	Q81W94	081w94 homo sapien
99	237	11.8	1260	2	Q72VY5	072vy5 mus musculu
100	236.5	11.8	1260	3	Q72VY5	072vy5 mus musculu
101	236.5	11.8	2570	1	SBN1_HUMAN	0973m1 gliardia lam
102	236	11.8	2570	2	SBN1_HUMAN	0973m1 gliardia lam
103	236	11.8	590	2	Q8C0B8	08c0b8 mus musculu
104	236	11.8	913	2	PECK5_HUMAN	09wuh9 ratu8 norv

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105	236	11.8	961	2	09BQC6	09eqc1 mus musculus	178	218.5	10.9	2516	2	07T052	07tcq2 mus musculus
106	236	11.8	1972	2	08WPL1	08wpl1 olkopleura	179	218.5	10.9	2526	2	07T051	07tcq1 mus musculus
107	236	11.8	2524	2	09GPAS	09gpas5 branchiosteo	180	218.5	10.9	2531	2	08K428	08k428 mus musculus
108	235.5	11.7	576	2	09YJVT	09y3v7 homo sapien	181	218.5	10.9	2531	2	07T050	07tcq0 mus musculus
109	235.5	11.7	1222	2	07PPC0	07ppc0 anopheles g	182	218	10.9	2471	1	NTC1_PAT	NTC1_PAT
110	234	11.6	1056	2	07A94	07a94 caenorhabd g	183	218	10.9	2471	1	NTC1_PAT	NTC1_PAT
111	233	11.6	992	2	08E029	08e029 homo sapien	184	218	10.9	2471	1	NTC1_PAT	NTC1_PAT
112	233	11.6	992	2	08E029	08e029 homo sapien	185	218	10.9	2471	1	NTC1_PAT	NTC1_PAT
113	232	11.6	992	2	08E029	08e029 homo sapien	186	218	10.9	2471	1	NTC1_PAT	NTC1_PAT
114	232	11.6	969	2	08IY28	08iy28 homo sapien	187	217.5	10.8	1095	2	060784	060784 mus musculus
115	232	11.6	1375	1	NTD1_HUMAN	014112 homo sapien	188	217.5	10.8	1242	1	JMGI_BRABE	JMGI_BRABE
116	232	11.6	1398	2	06APX6	06apx6 mus musculus	189	217.5	10.8	3704	2	08BTV4	08b183 giardia lam
117	231.5	11.5	827	2	06BPC9	06bpc9 mus musculus	190	217.5	10.8	3704	2	08BTV4	08b183 giardia lam
118	231.5	11.5	962	2	09UP98	09up98 mus musculus	191	216.5	10.8	327	2	08BTV4	08b183 giardia lam
119	231.5	11.5	993	2	066PY1	066py1 mus musculus	192	216.5	10.8	327	2	08BTV4	08b183 giardia lam
120	231	11.5	500	2	0664U4	0664u4 bos taurus	193	216.5	10.8	327	2	08BTV4	08b183 giardia lam
121	231	11.5	578	2	0912D3	0912d3 mus musculus	194	216.5	10.8	327	2	08BTV4	08b183 giardia lam
122	230.5	11.5	1399	2	08U130	08u130 xenopus lae	195	216	10.8	2673	1	066EFC	066e33 mus musculus
123	230.5	11.5	1399	2	08U130	08u130 xenopus lae	196	216	10.8	2673	1	066EFC	066e33 mus musculus
124	229.5	11.5	1399	2	08U130	08u130 xenopus lae	197	216	10.8	2673	1	066EFC	066e33 mus musculus
125	229.5	11.5	1399	2	08U130	08u130 xenopus lae	198	216	10.8	2673	1	066EFC	066e33 mus musculus
126	229.5	11.4	880	2	08NNU9	08nnu9 homo sapien	199	215.5	10.7	1317	2	061050	061050 mus musculus
127	229.5	11.4	1114	2	075WQ2	075wq2 penaeus jap	200	215	10.7	2471	1	NTC2_HUMAN	NTC2_HUMAN
128	229	11.4	674	2	070WP1	070wp1 giardia lam	201	215	10.7	1246	1	07P9Q4	07p9q4 anopheles g
129	228.5	11.4	649	1	PTES_MACHU	028530 maccaca mla	202	214.5	10.7	448	1	07P9Q4	07p9q4 anopheles g
130	228.5	11.4	886	1	EMR1_HUMAN	090y54 mus musculus	203	214.5	10.7	448	1	07P9Q4	07p9q4 anopheles g
131	228.5	11.4	1213	1	JMGI_BRABE	090y54 mus musculus	204	214.5	10.7	448	1	07P9Q4	07p9q4 anopheles g
132	228	11.4	1218	1	JMGI_BRABE	090y54 mus musculus	205	214.5	10.7	448	1	07P9Q4	07p9q4 anopheles g
133	228	11.4	1218	1	JMGI_BRABE	090y54 mus musculus	206	214.5	10.7	448	1	07P9Q4	07p9q4 anopheles g
134	226.5	11.3	1679	1	PMR2_DROME	P10432 drosophila	207	213.5	10.6	978	1	08E013	08e013 mus musculus
135	226.5	11.3	1679	1	PMR2_DROME	P10432 drosophila	208	213.5	10.6	978	1	08E013	08e013 mus musculus
136	226.5	11.3	1679	1	PMR2_DROME	P10432 drosophila	209	213.5	10.6	978	1	08E013	08e013 mus musculus
137	226	11.3	592	2	091XLS	091x15 mus musculus	210	213	10.6	674	1	08E013	08e013 mus musculus
138	226	11.3	592	2	091XLS	091x15 mus musculus	211	212.5	10.6	674	1	08E013	08e013 mus musculus
139	225.5	11.2	2531	1	NTC1_MOUSE	001705 mus musculus	212	212.5	10.6	674	1	08E013	08e013 mus musculus
140	225.5	11.2	1214	2	090YD2	090y42 xenopus lae	213	212.5	10.6	674	1	08E013	08e013 mus musculus
141	225	11.2	650	2	016519	016519 homo sapien	214	212.5	10.6	674	1	08E013	08e013 mus musculus
142	225	11.2	1018	2	06NZL6	06nzl6 mus musculus	215	212	10.6	674	1	08E013	08e013 mus musculus
143	224.5	11.2	608	2	080V54	080v54 mus musculus	216	212	10.6	674	1	08E013	08e013 mus musculus
144	224.5	11.2	1394	2	08C622	08c622 mus musculus	217	211.5	10.5	396	2	08E013	08e013 mus musculus
145	224.5	11.2	1403	2	NTD2_MOUSE	086352 mus musculus	218	211.5	10.5	396	2	08E013	08e013 mus musculus
146	224.5	11.2	1403	2	NTD2_MOUSE	086352 mus musculus	219	211.5	10.5	396	2	08E013	08e013 mus musculus
147	224.5	11.2	1403	2	NTD2_MOUSE	086352 mus musculus	220	211.5	10.5	396	2	08E013	08e013 mus musculus
148	224.5	11.2	1403	2	NTD2_MOUSE	086352 mus musculus	221	211.5	10.5	396	2	08E013	08e013 mus musculus
149	224.5	11.2	1574	2	08CPA3	08cpa3 mus musculus	222	211	10.5	931	1	EMR1_MOUSE	08e154 mus musculus
150	224.5	11.2	2447	2	013149	013149 fugu rubrip	223	211	10.5	931	1	EMR1_MOUSE	08e154 mus musculus
151	224	11.2	1219	1	JMGI_PAT	063722 rattus norv	224	211	10.5	931	1	EMR1_MOUSE	08e154 mus musculus
152	223	11.1	650	2	09NSD0	09nsd0 homo sapien	225	211	10.5	931	1	EMR1_MOUSE	08e154 mus musculus
153	223	11.1	1519	1	08WPN0	08wpm0 olkopleura	226	210.5	10.5	517	2	06X1W9	06x1w9 mus musculus
154	223	11.1	2524	2	NTC1_XENLA	P21783 xenopus lae	227	210.5	10.5	517	2	06X1W9	06x1w9 mus musculus
155	223	11.1	535	2	07Q023	07q023 anopheles g	228	210	10.5	517	2	06X1W9	06x1w9 mus musculus
156	222.5	11.1	1441	2	076X89	076x89 homo sapien	229	210	10.5	517	2	06X1W9	06x1w9 mus musculus
157	222.5	11.1	1441	2	076X89	076x89 homo sapien	230	210	10.5	517	2	06X1W9	06x1w9 mus musculus
158	222.5	11.1	1441	2	076X89	076x89 homo sapien	231	210	10.5	517	2	06X1W9	06x1w9 mus musculus
159	222.5	11.1	4007	2	075N88	075n88 homo sapien	232	210	10.5	517	2	06X1W9	06x1w9 mus musculus
160	222	11.1	347	2	09DDR4	09ddr4 gallus galli	233	209.5	10.4	448	1	07QXK6	07qxk6 mus musculus
161	222	11.1	675	2	09DDR4	09ddr4 gallus galli	234	209.5	10.4	448	1	07QXK6	07qxk6 mus musculus
162	222	11.1	838	2	018761	018761 caenorhabd1	235	209.5	10.4	448	1	07QXK6	07qxk6 mus musculus
163	222	11.1	838	2	018761	018761 caenorhabd1	236	209.5	10.4	448	1	07QXK6	07qxk6 mus musculus
164	222	11.1	1212	1	NTC1_PAT	027422 caenorhabd1	237	209.5	10.4	448	1	07QXK6	07qxk6 mus musculus
165	222	11.1	2556	1	NTC1_HUMAN	000918 rattus norv	238	209.5	10.4	448	1	07QXK6	07qxk6 mus musculus
166	221	11.0	1247	1	NTD0_HUMAN	P45531 homo sapien	239	209	10.4	448	1	07QXK6	07qxk6 mus musculus
167	221	11.0	2470	1	NTC1_MOUSE	P13553 mus musculus	240	209	10.4	448	1	07QXK6	07qxk6 mus musculus
168	220.5	11.0	1247	1	NTC1_MOUSE	P13553 mus musculus	241	209	10.4	448	1	07QXK6	07qxk6 mus musculus
169	220.5	11.0	1247	1	NTC1_MOUSE	P13553 mus musculus	242	209	10.4	448	1	07QXK6	07qxk6 mus musculus
170	220.5	11.0	1247	1	NTC1_MOUSE	P13553 mus musculus	243	209	10.4	448	1	07QXK6	07qxk6 mus musculus
171	220	11.0	913	2	08AV18	08av18 rana esculie	244	208.5	10.4	443	1	09XJ37	09xj37 mus musculus
172	220	11.0	913	2	08AV18	08av18 rana esculie	245	208.5	10.4	443	1	09XJ37	09xj37 mus musculus
173	220	11.0	1062	2	060789	060789 mus musculus	246	208	10.4	443	1	09XJ37	09xj37 mus musculus
174	220	11.0	2531	1	NTC1_PAT	007008 rattus norv	247	207	10.3	443	2	09J066	09j066 mus musculus
175	220	11.0	3623	2	070244	070244 rattus norv	248	207	10.3	443	2	09J066	09j066 mus musculus
176	218.5	10.9	461	2	P97883	P97883 rattus norv	249	207	10.3	443	2	09J066	09j066 mus musculus
177	218.5	10.9	1025	2	07R637	07r637 giardia lam	250	207	10.3	443	2	09J066	09j066 mus musculus

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103	109	9.4	1687	2	T30176	EGF repeat craneano
104	108.5	9.4	9922	2	152527	PAGE4 - mouse (fr
105	108.5	9.4	3566	1	A40701	tenascin-X precurs
106	108	9.4	999	1	A39450	tenascin-X-like pr
107	108	9.4	1111	2	T6972	hypothetical prote
108	107.5	9.4	4543	1	A53232	tenascin alpha-1 ch
109	108	9.4	741	2	T46468	hypothetical prote
110	107.5	9.4	937	2	T53282	gene PACS3 protein
111	107.5	9.4	385	2	S53718	homocysteine protei
112	107	9.3	385	2	S53718	homocysteine protei
113	107	9.3	385	2	S53718	homocysteine protei
114	106	9.3	621	2	T38467	low density lipopr
115	105.5	9.3	511	2	T17298	hypothetical prote
116	105	9.2	1207	1	EGHU	epidermal growth f
117	105	9.2	1650	2	S53457	dominant autointg
118	105	9.2	1810	1	A12230	tenascin precursor
119	105	9.2	1810	1	A12230	tenascin precursor
120	105	9.2	1810	1	A12230	tenascin precursor
121	105	9.2	1810	1	A12230	tenascin precursor
122	103.5	9.2	558	2	T17124	hypothetical prote
123	103	9.1	1395	2	A32901	glp1 protein precu
124	103	9.1	1790	1	MMFPI	tenascin beta-1 cha
125	103	9.1	4753	1	A47437	LDL-receptor-relat
126	102.5	9.1	782	2	A61635	tenascin-like prote
127	102.5	9.1	1372	2	T25933	hypothetical prote
128	102.5	9.1	1746	1	S14694	tenascin precursor
129	102.5	9.1	3075	2	S14694	tenascin precursor
130	101.5	9.1	3075	2	S14694	tenascin precursor
131	101.5	9.1	3075	2	S14694	tenascin precursor
132	101.5	9.1	3075	2	S14694	tenascin precursor
133	101.5	9.1	3075	2	S14694	tenascin precursor
134	100.5	9.0	1081	2	T31329	tenascin-C - huma
135	100.5	9.0	2201	2	A32160	alpha-2-macroglobu
136	100.5	9.0	4545	1	S25111	gene secret prote
137	100.5	9.0	1408	2	S16148	tenascin precursor
138	100.5	9.0	2019	1	J01322	tenascin alpha-1 ch
139	100.5	9.0	3084	1	MMFSA	epidermal growth f
140	100.5	9.0	3084	1	MMFSA	epidermal growth f
141	100.5	9.0	3084	1	MMFSA	epidermal growth f
142	100.5	9.0	3084	1	MMFSA	epidermal growth f
143	100.5	9.0	3084	1	MMFSA	epidermal growth f
144	100.5	9.0	3084	1	MMFSA	epidermal growth f
145	100.5	9.0	3084	1	MMFSA	epidermal growth f
146	100.5	9.0	3084	1	MMFSA	epidermal growth f
147	100.5	9.0	3084	1	MMFSA	epidermal growth f
148	100.5	9.0	3084	1	MMFSA	epidermal growth f
149	100.5	9.0	3084	1	MMFSA	epidermal growth f
150	100.5	9.0	3084	1	MMFSA	epidermal growth f
151	100.5	9.0	3084	1	MMFSA	epidermal growth f
152	100.5	9.0	3084	1	MMFSA	epidermal growth f
153	100.5	9.0	3084	1	MMFSA	epidermal growth f
154	100.5	9.0	3084	1	MMFSA	epidermal growth f
155	100.5	9.0	3084	1	MMFSA	epidermal growth f
156	100.5	9.0	3084	1	MMFSA	epidermal growth f
157	100.5	9.0	3084	1	MMFSA	epidermal growth f
158	100.5	9.0	3084	1	MMFSA	epidermal growth f
159	100.5	9.0	3084	1	MMFSA	epidermal growth f
160	100.5	9.0	3084	1	MMFSA	epidermal growth f
161	100.5	9.0	3084	1	MMFSA	epidermal growth f
162	100.5	9.0	3084	1	MMFSA	epidermal growth f
163	100.5	9.0	3084	1	MMFSA	epidermal growth f
164	100.5	9.0	3084	1	MMFSA	epidermal growth f
165	100.5	9.0	3084	1	MMFSA	epidermal growth f
166	100.5	9.0	3084	1	MMFSA	epidermal growth f
167	100.5	9.0	3084	1	MMFSA	epidermal growth f
168	100.5	9.0	3084	1	MMFSA	epidermal growth f
169	100.5	9.0	3084	1	MMFSA	epidermal growth f
170	100.5	9.0	3084	1	MMFSA	epidermal growth f
171	100.5	9.0	3084	1	MMFSA	epidermal growth f
172	100.5	9.0	3084	1	MMFSA	epidermal growth f
173	100.5	9.0	3084	1	MMFSA	epidermal growth f
174	100.5	9.0	3084	1	MMFSA	epidermal growth f
175	100.5	9.0	3084	1	MMFSA	epidermal growth f

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